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REMARKS

Claims 1-4, 6-8, 10-16 and 23-26 are pending in the above-referenced application. Claim 9 has been canceled without prejudice. Applicant reserves the right to file subsequent continuation and/or divisional applications on canceled subject matter.

Claims 27-29 have been added to recite specific uses of the claimed sequences. Specifically, claim 27 is directed to a method of identifying a nucleotide sequence variant of SEQ ID NO:8; claim 28 depends from claim 27. Claim 29 is directed to a method of detecting the presence or absence of SEQ ID NO:8 in a sample. New claims 27-29 are supported by the specification (see, e.g. page 31, lines 3-12 in substitute specification).

The specification on page 20, lines 22-30 has been amended to correct a typographical error which has heretofore gone unnoticed. Specifically AEBP gene is recited to be located between nucleotides 1301-10893 of SEQ ID NO:8 as shown in Table 2 on pages 13 and 14. No new matter has been added by this claim amendment

Applicant would like to thank Examiner J. Zara for her time and most helpful suggestions during her interview with Applicant's representative, Cheryl H. Agris on April 12, 2007. As discussed, claim 1 has been amended to be directed to a nucleic acid molecule of SEQ ID NO:8 or a fragment thereof comprising nucleotides 1301-10893 of SEQ ID NO:8, both of which encode a polypeptide having human adipocyte enhancer binding protein 1 activity and the complement of either of these. Amended claim 1 is supported by the specification at Table 2 and page 20, lines 22-30 (of substitute specification-see above).

Claim 8 has been amended to be directed to a nucleic acid molecule at least 20 contiguous nucleotides **identical** to an intron region specific to the nucleic acid molecule recited in claim 1. Amended claim 8 is supported by the specification. For example, on page 31, lines 7-12 (see substitute specification), it is stated:

> Polynucleotides containing noncoding regions may be used as PCR primers and may be used to amplify the genomic DNA isolated from the patients. Additionally, primers may be obtained by routine or long range PCR, that can yield products containing more than one exon and intervening intron. The sequence of the amplified genomic DNA from the patient may be determined using methods known in the art. Such probes may be between 10-100 nucleotides in length and may preferably be between 20-50 nucleotides in length.

During the interview, the Examiner specifically requests that specific introns be designated for search purposes. In response, Applicant designates intron 1 (10642-9015)), intron 2 (nucleotides 8674-8122), intron 6 (7477-6662) and/or intron 9 (nucleotides 6273-5546).

1. The Rejections Under 35 USC §112, First Paragraph

Claims 1-4, 6, 8, 10, 11 and 14-16 have been rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The Office Action specifically asserts:

> The claims are drawn to compositions comprising isolated genomic nucleic acid molecules having a nucleotide sequence at least 95% identical to any polynucleotide encoding the polypeptide of SEQ ID NO. 3, or any nucleic acid molecule that hybridizes to these polynucleotides, and isolated nucleic acids comprising at least 20 nucleotides that hybridize with high stringency to an intronic region of SEQ ID No. 6.
>
> The specification, claims and the art do not adequately describe the distinguishing features or attributes concisely shared by the members of the genus comprising these nucleic acids that are at least 95% homologous to any polynucleotide that encodes the polypeptide of SEQ ID NO. 3, or nucleic acids that specifically hybridize to them, or any polynucleotide that stringently hybridizes to the intronic sequences of SEQ ID No. 6. The specification teaches the sequence of SEQ ID No. 6, encoding the polypeptide of SEQ ID NO. 3. The genus of nucleic acids claimed, however, encompasses a myriad of structures *(e.g.* thousands and thousands of nucleic acid sequences) and the specification and claims do not adequately teach a representative number of species for the broad genus claimed, and which provide for the function claimed, of having human adipocyte enhancer binding protein 1 activity.
>
> Concise structural features that could distinguish structures within the genus from others are missing from the disclosure. No common structural attributes identify the members of the claimed genus, and distinguish members within the claimed genus from those outside of it, and which provide for the function claimed, of having human adipocyte enhancer binding protein 1 activity. One of skill in the art would reasonably conclude that the disclosure fails to provide a representative number of species to describe the genus claimed.

Applicant respectfully traverses the rejection. However, in order to advance prosecution, claim 1 has been amended to be directed to (a) a genomic nucleic acid molecule which is the nucleic acid molecule of SEQ ID NO:8; (b) fragment of (a) comprising nucleotides 1301-10893

of SEQ ID NO:8 or (c) a complement of (a) or (b). As noted above, amended claim 1 is supported by the specification, particularly in Table 2 and page 20. Claims 2-4, 6, 8, 10, 11 and 14-16 depend from claim 1. Therefore, arguments made with respect to claim 1 apply here as well.

In view of the amendments of claims 1 and 8 and the above arguments, Applicant asserts that the rejection under 35 USC 112, first paragraph has been overcome. Therefore, Applicant respectfully requests that the rejection be withdrawn.

2. The Rejections Under 35 USC 102

2.1 Layne et al.

Claims 1-4, 6 and 10 are rejected under 35 U.S.C. 102(b) as being anticipated by Layne et al. Specifically, it is asserted

> Layne et al (J. Biol. Chem., Vol. 273, No. 25, pages 15,654-15,660, 1998) teach compositions and methods of recombinant polypeptide expression in vitro comprising the nucleic acid encoding the polypeptide of SEQ ID NO. 3 and further comprising a carrier (e.g. water), as well as an expression vector and recombinant host cells comprising the nucleic acid encoding the polypeptide of SEQ ID No. 3 (see the abstract on p. 15,654, text on p. 15,655, fig. 1 on p. 15,656, discussion on pp. 15,658-9. See also the accompanying alignment between SEQ ID No. 3 of the instant application and AF053944 of Layne et al).

Applicant traverses the rejection. However, in order to advance prosecution, claim 1 has been amended to more distinctly claim that which Applicant regards as the invention. Specifically, claim 1 recites that at a minimum the nucleic acid molecule is a genomic nucleic acid molecule that comprises nucleotides 1301-10893 of SEQ ID NO:8. This sequence encodes a polypeptide having human adipocyte enhancer binding protein 1 activity (e.g., SEQ ID NO:3). The claimed sequence however contains both exon and intron regions. In contrast, Layne discloses a cDNA encoding human adipocyte enhancer binding protein 1 activity but does not contain any noncoding sequences. Specifically, the cDNA disclosed in Layne only contains exon sequences. Thus, amended claim 1 would not be anticipated by Layne et al.

Claims 2-4, 6 and 10 depend from claim 1. Therefore, arguments made with respect to claim 1 would be applicable to claims 2-4, 6 and 10.

In view of the amendment of claim 1 and the above arguments, Applicant assert that the rejection over claims 1-4, 6 and 10 over Layne et al. under 35 USC 102(b) have been overcome. Therefore, Applicant respectfully requests that the rejections under 35 USC 102(b) over claims 1-4, 6 and 10 over Layne et al. be withdrawn.

2.2. Noonberg et al.

Claims 8 and 11 are rejected under 35 U.S.C. 102(b) as being anticipated by Noonberg et al.

> Noonberg et al (USPN 5,624,803) teach compositions comprising a polynucleotide at least 20 nucleobases in length that specifically hybridizes under stringent condition with an intronic sequence of SEQ ID NO. 6 and further comprising a carrier, water (see the accompanying sequence alignment data between nucleotides 3002-3237 of SEQ ID NO. 6 and SEQ ID No. 20 of Noonberg et al. In the alignment data, nucleotide no. 3002 of SEQ ID No. 6 = nucleotide no. 1).

Applicant respectfully traverses the rejection. However, in order to advance prosecution, Applicant has amended claims 1 and 8. As noted above, claim 1 has been amended to recite that the nucleotide sequence comprises at least nucleotides 1301-10893 of SEQ ID NO:8. Claim 8 has been amended to recite that the acid molecule of at least 20 contiguous nucleotides identical to an intron region specific to the nucleic acid molecule of claim 1. There is no disclosure in Noonberg et al. of a 20 contiguous nucleotide fragment identical to an intron region of SEQ ID NO:8. Therefore, amended claim 8 is not anticipated by Noonberg et al.

Claim 11 depends from claim 8. Therefore, arguments made with respect to claim 8 would be applicable to claim 11.

In view of the amendment of claims 1 and 8 and the above arguments, Applicant asserts that the rejection over claims 8 and 11 over Noonberg et al. under 35 USC 102(b) have been overcome. Therefore, Applicant respectfully requests that the rejections under 35 USC 102(b) over claims 8 and 11 over Noonberg et al. be withdrawn.

2.3 Denney et al.

Claims 8 and 11 are rejected under 35 U.S.C. 102(e) as being anticipated by Denney et al. Specifically, it is asserted in the Office Action:

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Denney et al (USPN 5,972,334) teach a compositions comprising a polynucleotide at least 20 nucleobases in length that specifically hybridizes under stringent condition with an intronic sequence of SEQ ID NO. 6 and further comprising a carrier, water (see the accompanying sequence alignment data between nucleotides 1967-2208 of SEQ ID NO. 6 and SEQ ID No. 35 of Denney et al. In the alignment data, Nucleotide no. 3002 of SEQ ID No. 6 = nucleotide no. 1).

Applicant respectfully traverses the rejection. However, in order to advance prosecution, Applicant has amended claims 1 and 8. As noted above, claim 1 has been amended to recite that the nucleotide sequence comprises at least nucleotides 1301-10893 of SEQ ID NO:8. Claim 8 has been amended to recite that the acid molecule of at least 20 contiguous nucleotides identical to an intron region specific to the nucleic acid molecule of claim 1. There is no disclosure in Denny et al. of a 20 contiguous nucleotide identical to an intron region of SEQ ID NO:8. Therefore, amended claim 8 is not anticipated by Denny et al.

Claim 11 depends from claim 8. Therefore, arguments made with respect to claim 8 would be applicable to claim 11.

In view of the amendment of claims 1 and 8 and the above arguments, Applicant asserts that the rejection over claims 8 and 11 over Denny et al. under 35 USC 102(b) have been overcome. Therefore, Applicant respectfully requests that the rejections under 35 USC 102(b) over claims 8 and 11 over Denny et al. be withdrawn.

3. Conclusion

In view of the foregoing, Applicants assert that the claims are now in condition for allowance. Early action to that end is respectfully requested. The Examiner is invited to contact the undersigned at (914) 712-0093 if he has any questions.

Respectfully submitted,

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